

SEQUENCE LISTING

<110> Cahoon, Rebecca E.
Fang, Yiwen
Odell, Joan
Weng, Zude

<120> Plant Myb Transcription Factor Homologs

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<151> 1998-December-02

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 Val Ser Tyr Ile Ser Gln His Gly Glu Gly Ser Trp Asp Asn Leu Ala
 35 40 45
 Arg Ala Ala Gly Leu Asn Arg Asn Gly Lys Ser Cys Arg Leu Arg Trp
 50 55 60
 Leu Asn Tyr Leu Arg Pro Gly Val Arg Arg Gly Ser Ile Thr Ala Gly
 65 70 75 80
 Glu Asp Thr Val Ile Arg Glu Leu His Ala Arg Trp Gly Asn Lys Trp
 85 90 95
 Ser Lys Ile Ser Lys His Leu Pro Gly Arg Thr Asp Asn Glu Xaa Lys
 100 105 110
 Asn Tyr Trp Arg Thr Arg Ile Gln Gln Glu Glu Gln Gln Gly Ala Lys
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 Asp Asp Tyr Trp Val His Asn Pro Thr Pro Thr Thr Ser
 145 150 155

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35 40 45
Cys Arg Leu Arg Trp Val Asn Tyr Leu His Pro Gly Leu Lys Arg Gly
50 55 60
Arg Met Ser Pro His Glu Glu Arg Leu Ile Leu Glu Leu His Ala Arg
65 70 75 80
Trp Gly Asn Arg Trp Ser Arg Ile Ala Arg Arg Leu Pro Gly Arg Thr
85 90 95
Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr His Met Arg Lys Lys Ala
100 105 110
Gln Glu Arg Lys Arg Asn Met Ser Pro Ser Ser Ser Ser Ser Leu
115 120 125
Ser Tyr Gln Ser Gly Tyr Pro Asp Thr Pro Ser Ile Ile Gly Val Lys
130 135 140
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 35 40 45
 Asn Tyr Leu Arg Pro Asp Val Lys Arg Gly Asn Phe Ser Ala Asp Glu
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cagccaccag ctgaaggagg gagcgagga ggaggtgag aacgacaata ataagccgga 240
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 35          40          45

Asp Asn Asn Lys Pro Glu Leu Arg Arg Gly Pro Trp Thr Val Asp Glu
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Asp Leu Thr Leu Val Asn Tyr Ile Ala Asp Asn Gly Glu Gly Arg Trp
 65          70          75          80

Asn Asn Leu Ala Arg Ala Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys
 85          90          95

Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Lys Arg Gly Asn
100          105          110

Phe Ser Ala Asp Glu Gln Leu Leu Ile Leu Asp Leu His Thr Arg Trp
115          120          125

Gly Asn Arg Trp Ser Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp
130          135          140

Asn Glu Ile Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys
145          150          155          160

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Ala Asn Asp Asp Asp Glu Asp His His His Asn Leu Arg Leu Leu Val
195 200 205

Leu His His His Gln Ala Gln His Leu Gln Gln Ala Ala Ala Ala Ala
210 215 220

Gly Gly Ala Ala Asn Asp Leu Ala Ala Gly Ala Tyr Asp Val Arg Gln
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Leu His Ala Leu Pro Ser Ser Gly Met Ala Ala Thr Ser Ser Ser Asp
245 250 255

Ser Leu Ala Ser Glu Ser Tyr Asp Asp Gly Gly Leu Leu Phe Ala Asn
260 265 270

Leu Arg Ala Gly Glu Met Leu Met Asp Gly Gly Asp Trp Ala Ala Gln
275 280 285

Gln Glu Ala Asp Gln Gly Leu Trp Pro Pro Pro Pro Pro Pro Ser
290 295 300

Asp Leu Asp Gln Ser Val Val Gln Ala Ala Gly Ala Gly Ala Gly Gln
305 310 315 320

Phe Gln Asp Met Glu Leu Ser Gly Trp Val Gln Gly Phe Ser Glu Ser
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<213> Oryza sativa

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Ser Cys Arg Leu Arg Trp Val Asn Tyr Leu His Pro Gly Leu Lys Arg
20 25 30

Gly Arg Met Ser Pro Glu Glu Glu Arg Met Val Val Gln Leu His Ala
35 40 45

Lys Leu Gly Asn Arg Trp Ser Arg Ile Ala Lys Ser Ile Pro Gly Arg
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Thr Asp Asn Glu Ile Lys Asn
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<213> Oryza sativa

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Ser Gly Leu Gln Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Val Asn
35 40 45

Tyr Leu His Pro Gly Leu Lys Arg Gly Arg Met Ser Pro Glu Glu Glu
50 55 60

Arg Met Val Val Gln Leu His Ala Lys Leu Gly Asn Arg Trp Ser Arg
65 70 75 80

Ile Ala Lys Ser Ile Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr
85 90 95

Trp Arg Thr His Leu Arg Lys Leu Lys Leu Lys Gln Gln Lys Gln Gln
100 105 110

Gln Ser Asp Asp His His Asn Asp Asn Asp Asp Asp Asp Arg Asn
115 120 125

Ser Ser Ser Ser Ser Ser Ser Ser Asn Ser Asn Ser Asn Leu Gln Gln
130 135 140

Gln Pro Gln Pro Glu Asp Glu Ser Ser Ala Ser Gly Ser Leu Gln Ala
145 150 155 160

Gln His His Glu Asp Gln His Gln Leu Phe Leu His Pro Leu Trp Asn
165 170 175

Asp Asp Ile Ile Val Asp Val Asp Cys Trp Ser Ser Ser Thr Asn Val
180 185 190

Val Ala Pro Pro Pro Met Pro Ala Ser Pro Leu Trp Asp Ile Asp Asp
195 200 205

Ala Phe Phe Cys Ser Asp Tyr Ser Leu Pro Leu Trp Gly
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 35 40 45

Gly Lys Ser Cys Arg Leu Arg Trp Val Asn Xaa Leu Gln Pro
 50 55 60

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Asp Glu Leu Arg Arg Gly Pro Trp Thr Val Glu Glu Asp Leu Leu Leu
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Val Asn Tyr Ile Ala Ala His Gly Glu Gly Arg Trp Asn Ala Leu Ala
 35 40 45

Arg Cys Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp
 50 55 60

Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Met Thr Ala Glu
 65 70 75 80

Glu Gln Leu Leu Ile Leu Glu Leu His Gly Arg Trp Gly Asn Arg Trp
 85 90 95

10021811 "121401

Ser Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys
100 105 110

Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys His Leu Asn Cys
115 120 125

Asp Val Asn Ser Gln Gln Phe Lys Asp Leu Met Arg Tyr Leu Trp Met
130 135 140

Pro
145

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20 25 30

Gln Leu Leu Ile Leu Asp Leu His Ser Arg Trp Gly Asn Arg Trp Ser
35 40 45

Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asp Glu Ile Lys Asn
50 55 60

Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu Asn Cys Asp
65 70 75 80

Val Asn Ser Lys Arg Phe Lys Asp Ala Met Lys Tyr Leu Trp Met Pro
85 90 95

Arg Leu Ala Glu Arg Ile His Ala Arg Ala Gly Ala Val Asp Asp Ser
100 105 110

Gly Asp Tyr Ser Asn Asn Asp Leu Ser Cys Val Ser Gly Val Thr Met
115 120 125

Ala Thr Val Ala Asn Cys Phe Asp Gly Ser Pro Ser Met Val Thr Ser
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Ser Ser
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<400> 21
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tctatccgat caatcgactg gcccgcgagg atcgatcgag actcgaaagg gagggatttt 180
gatccggatc ggtcgacgat ggacatggcg cacgagaggg acgagagcag cgaggaggag 240
gtgatgggcg gcgacctgcg tcgcgggccg tggacggtgg aggaggacct cctgctcgtc 300
aactacatcg ccgcgcacgg cgaggggccg tggaaactcg tcgcccgatc agcanggctg 360
aaacgcacag gcaagagctg ccggctccgg tggctgaact acctccgcc cgacctccgg 420
cgaggcaaca tcacgccgca agagcagctg ctcatcctgg agctgcactc gcggtgggga 480
aaccgctggt ccaagatngc gcagcacctc ccgggaagca ccgacaacga gatnaagaat 540
acnggcgcac gcggtgcaga agcaccgaag cagtcaagtg cnaactcaaca gcaacantta 600
aggacncatg cgctactcng gatgcccgt ctnagggat 640

<210> 22
<211> 115

<220>
 <221> unsure
 <222> (376)

 <220>
 <221> unsure
 <222> (381)

 <220>
 <221> unsure
 <222> (386)

 <220>
 <221> unsure
 <222> (393)

 <220>
 <221> unsure
 <222> (408) .. (409)

 <220>
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 <222> (432)

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 <222> (453)

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 <222> (466)

 <220>
 <221> unsure
 <222> (469)

 <220>
 <221> unsure
 <222> (476) .. (477)

<400> 23
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 ggggccatgg acgccggagg aggacctgat gctggctctcc tacatccagg agcacggcgc 180
 cggcaactgg cgcgccgtgc cgacgaacac cgggctgatg cgttgcagca agagctgccg 240
 gctccgggtg acgaactacc tcaggccggg gatcaagcgg gggaacttca ccgagcanga 300
 ggagaagctc atcgtccacc tccaggctct cctcggcaac cggtgggcaa cgatnncgtc 360
 gtacttgccg gganangacg ncaacnacat cangaatact gggaacannc acctcangaa 420
 gaactcaaga anatgcaagc caccggagggt ggngaaaaca gcgcgncgnc tcgganngtt 480
 gcgg 484

<210> 24
 <211> 126
 <212> PRT
 <213> Oryza sativa

<220>
 <221> UNSURE
 <222> (13)

<220>
 <221> UNSURE
 <222> (73)

<220>
 <221> UNSURE
 <222> (92) .. (93)

<220>
 <221> UNSURE
 <222> (99)

<220>
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 <222> (101)

<220>
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 <222> (113)

<220>
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 <222> (118)

<220>
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 <222> (125)

<400> 24
 Met Gly Arg Pro Pro Cys Cys Asp Lys Val Gly Val Xaa Lys Gly Pro
 1 5 10 15

Trp Thr Pro Glu Glu Asp Leu Met Leu Val Ser Tyr Ile Gln Glu His
 20 25 30

Gly Ala Gly Asn Trp Arg Ala Val Pro Thr Asn Thr Gly Leu Met Arg
 35 40 45

Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly
 50 55 60

Ile Lys Arg Gly Asn Phe Thr Glu Xaa Glu Glu Lys Leu Ile Val His
 65 70 75 80

Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Thr Xaa Xaa Ser Tyr Leu
85 90 95

Pro Gly Xaa Asp Xaa Asn Xaa Ile Xaa Asn Thr Gly Asn Xaa His Leu
100 105 110

Xaa Lys Asn Ser Arg Xaa Cys Lys Pro Pro Glu Val Xaa Lys
115 120 125

<210> 25
<211> 1427
<212> DNA
<213> Oryza sativa

<400> 25
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tgaagaagg gccatggagc ccggaggagg acctgatgct ggtctcctac atccaggagc 180
acggcgccgg caactggcgc gccgtgccga cgaacaccgg gctgatgcgt tgcagcaaga 240
gctgccggct ccggtggagc aactacctca ggccggggat caagcggggg aacttcaccg 300
agcaggagga gaagctcatc gtccacctcc aggtctctct cggcaaccgg tgggcagcga 360
tagcgctcgt cttgccggag aggacggaca acgacatcaa gaactactgg aacacgcacc 420
tcaagaagaa gctcaagaag atgcaggccg ccggagggtg ggaagacagc ggccgcgcct 480
cggagggtgg cggcggccgc ggcgacggcg acggcgggcg gaaaagcgtg aaggccgccg 540
cacctaagg gcagtgggag cggcggtgct agacggacat ccacacggcg cggcaggcgc 600
tgccgcgacg gctctcgtc gaccaccccc acccgctgcc ggcgacggcg gcggcgccgc 660
cgacgccagc ggggtcgtcg gcggcgtagc cgtcgagcgc ggacaacatc gcgcggctgc 720
tgcagggtcg gatgcgccc ggcgcgggcg gcggcgggcaa cggcaagggc cccgaggcgt 780
cggggtcgac ctccacgagc gcgacgagc agcagcagcc gcagtgtctc ggcgaggggc 840
cggcatccgc gtccgcgtcg gcgagccaga gcggcgccgc cgcgcggcg actgcccaga 900
cgccggagtg ctcgacggag acgagcaaga tggccaccgg cggcgggcgcc ggcgggcccc 960
cgccggcggt ctcgatgct gagagctggc tgctcgacga cggcgggcat gggtcctatg 1020
acgtggtgcc attgggggac cccagttagt tcttttaagt gtagtacaac caaaattaaa 1080
ttaatcaagt agacagcaag aacaaaaaaaa aataatggaa agttgccgag ttaattaatc 1140
aagatgcaac taatcaaagc taattaaaag ggcttcgagt taattctcgg tgattttaat 1200
cgagtttgca ggtgttgatc tagcttggtt aattaatcct ttcttttgta ggtttttagt 1260
taattagtct ctctgatgat gctagggttt ggaactgac atagttaagt taatttatac 1320
taatggtagg cctgtgactt gtgattagtt agtcctgagt ggataaataa agacataaat 1380
gtacatcttt ttaaaagata aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1427

<210> 26
<211> 323
<212> PRT
<213> Oryza sativa

<400> 26
Met Gly Arg Pro Pro Cys Cys Asp Lys Val Gly Val Lys Lys Gly Pro
1 5 10 15

Trp Thr Pro Glu Glu Asp Leu Met Leu Val Ser Tyr Ile Gln Glu His
20 25 30

Gly Ala Gly Asn Trp Arg Ala Val Pro Thr Asn Thr Gly Leu Met Arg
35 40 45

Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly
50 55 60

Ile Lys Arg Gly Asn Phe Thr Glu Gln Glu Glu Lys Leu Ile Val His
 65 70 75 80
 Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu
 85 90 95
 Pro Glu Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr His Leu
 100 105 110
 Lys Lys Lys Leu Lys Lys Met Gln Ala Ala Gly Gly Gly Glu Asp Ser
 115 120 125
 Gly Ala Ala Ser Glu Gly Gly Gly Gly Arg Gly Asp Gly Asp Gly Gly
 130 135 140
 Gly Lys Ser Val Lys Ala Ala Ala Pro Lys Gly Gln Trp Glu Arg Arg
 145 150 155 160
 Leu Gln Thr Asp Ile His Thr Ala Arg Gln Ala Leu Arg Asp Ala Leu
 165 170 175
 Ser Leu Asp His Pro Asp Pro Ser Pro Ala Thr Ala Ala Ala Ala Ala
 180 185 190
 Thr Pro Ala Gly Ser Ser Ala Ala Tyr Ala Ser Ser Ala Asp Asn Ile
 195 200 205
 Ala Arg Leu Leu Gln Gly Trp Met Arg Pro Gly Gly Gly Gly Gly Gly
 210 215 220
 Asn Gly Lys Gly Pro Glu Ala Ser Gly Ser Thr Ser Thr Thr Ala Thr
 225 230 235 240
 Thr Gln Gln Gln Pro Gln Cys Ser Gly Glu Gly Ala Ala Ser Ala Ser
 245 250 255
 Ala Ser Ala Ser Gln Ser Gly Ala Ala Ala Ala Ala Thr Ala Gln Thr
 260 265 270
 Pro Glu Cys Ser Thr Glu Thr Ser Lys Met Ala Thr Gly Gly Gly Ala
 275 280 285
 Gly Gly Pro Ala Pro Ala Phe Ser Met Leu Glu Ser Trp Leu Leu Asp
 290 295 300
 Asp Gly Gly Met Gly Leu Met Asp Val Val Pro Leu Gly Asp Pro Ser
 305 310 315 320
 Glu Phe Phe

<210> 27
 <211> 557
 <212> DNA
 <213> Glycine max
 <220>
 <221> unsure
 <222> (136)

tggccaaaag ctgctgggtct caaacgtacc ggaaagattg ccggctaang tggctaaact 240
 acctccgtcc tgatgtaga agaggaata ntacacccga aggaacaact ttgatcatgg 300
 agcttcacgc aaagtgggga aacaggtggt ccaaaattgc caagcatcta cctggtagga 360
 cagtaatgag atnaagaact antggnggac aaggatcaga agcacatcaa gcaactgaga 420
 attnagcaac aatcacataa ctctgagata atgttacaag ctagatacca agttntacaa 480
 ggtgaaccat ggnnactatc ccaacctttt naaggaagtn angcatttct naatcnttcc 540
 ccaaataacc gnntatc 557

<210> 28
 <211> 94
 <212> PRT
 <213> Glycine max

<220>
 <221> UNSURE
 <222> (19)..(20)

<220>
 <221> UNSURE
 <222> (51)

<220>
 <221> UNSURE
 <222> (65)

<400> 28
 Ser Gln Asp Pro Glu Val Arg Lys Gly Pro Trp Thr Met Glu Glu Asp
 1 5 10 15
 Leu Ile Xaa Xaa Ile Asn Tyr Ile Ala Asn His Gly Glu Gly Val Trp
 20 25 30
 Asn Ser Leu Ala Lys Ser Cys Trp Ser Gln Thr Tyr Arg Lys Asp Cys
 35 40 45
 Arg Leu Xaa Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn
 50 55 60
 Xaa Thr Pro Glu Gly Thr Thr Leu Ile Met Glu Leu His Ala Lys Trp
 65 70 75 80
 Asn Arg Trp Ser Lys Ile Ala Lys His Leu Pro Gly Arg Thr
 85 90

<210> 29
 <211> 988
 <212> DNA
 <213> Glycine max

<400> 29
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 atggataaaa aacaactgtg caacacgtct caagatcctg aagtgagaaa aggaccttgg 120
 acgatggaag aagacttgat cttgatcaac tatattgcaa atcatgggga aggtggttgg 180
 aattctttgg ccaaagctgc tgggtctcaa cgtaccggaa agagttgccg gctaagggtg 240
 ctaaaactacc tccgtcctga tgtagaaga gggaatatta cacccgagga acaacttttg 300
 atcatggagc ttcacgcaaa gtggggaaac aggtggtcca aaattgccaa gcatctacct 360
 ggtaggacag ataatgagat caagaactat tggaggacca ggatccagaa gcacatcaag 420
 caagctgaga actttcagca acaaactcagc aataactctg agataaatga tcaccaagct 480
 agcactagcc atgtttctac catggctgaa cccatggaga cctattctcc acccttttat 540
 caaggaatgt tagagccatt ttcttcaatt cagttcccca caattaatcc tgatcaatcc 600

agttgttgta ccaatgacaa caacaacagc attaactatt ggagcatgga ggatatctgg 660
tcaatgcagt tactgaacgg ggattaaata ttgatataac aagataaacc taaattcctg 720
tataagttcc ataaaacact ggaatgtctc tggcttaaaa catattatta ttaggtttgt 780
ttatataagt agttggatat gtttggtttt gcgtaccatt attagcatat atatatatat 840
ttcaaagtga atgctatgtg cattgtaaaa gatatgggta agaaccacat agtttcaaaa 900
ctcttaataa taattccagt cacttattat aggaagtcta ttattaatta tctccaagat 960
gtttgcttaa aaaaaaaaaa aaaaaaaaaa 988

<210> 30
<211> 208
<212> PRT
<213> Glycine max

<400> 30
Met Asp Lys Lys Gln Leu Cys Asn Thr Ser Gln Asp Pro Glu Val Arg
1 5 10 15
Lys Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile
20 25 30
Ala Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly
35 40 45
Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu
50 55 60
Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu
65 70 75 80
Ile Met Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala
85 90 95
Lys His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg
100 105 110
Thr Arg Ile Gln Lys His Ile Lys Gln Ala Glu Asn Phe Gln Gln Gln
115 120 125
Ile Ser Asn Asn Ser Glu Ile Asn Asp His Gln Ala Ser Thr Ser His
130 135 140
Val Ser Thr Met Ala Glu Pro Met Glu Thr Tyr Ser Pro Pro Phe Tyr
145 150 155 160
Gln Gly Met Leu Glu Pro Phe Ser Ser Ile Gln Phe Pro Thr Ile Asn
165 170 175
Pro Asp Gln Ser Ser Cys Cys Thr Asn Asp Asn Asn Asn Ser Ile Asn
180 185 190
Tyr Trp Ser Met Glu Asp Ile Trp Ser Met Gln Leu Leu Asn Gly Asp
195 200 205

<210> 31
<211> 530
<212> DNA
<213> Glycine max

<220>
 <221> unsure
 <222> (301)

<220>
 <221> unsure
 <222> (356)

<220>
 <221> unsure
 <222> (388)

<220>
 <221> unsure
 <222> (393)

<220>
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 <222> (470)

<220>
 <221> unsure
 <222> (485)

<220>
 <221> unsure
 <222> (495)

<220>
 <221> unsure
 <222> (513)

<220>
 <221> unsure
 <222> (517)

<220>
 <221> unsure
 <222> (522)

<400> 31
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 tggaaactctt tggccaaggc tgctggactt aaacgtaccg gaaagagttg ccggctccgg 180
 tggctaaact acctccgtcc tgatgttaga agagggaata ttacacccga ggaacagctt 240
 ttgatcatgg aacttcatgc aaagtgggga aacagggtgt ccaaaattgc caagcatcta 300
 nccggaagga ctgataatga gattaagaac tactggagga caaggatcaa gaacantca 360
 agcaagcctt caacaacttc aacaacanag tantaattct gagataattt acatcccaag 420
 cttgcacaac caattgtcaa caatgggcaa cccaaaaaaa ctaatctcan caatttcaag 480
 gaagnttatt cattnaatca attccaaaaa ccncacntct antgtttcaa 530

<210> 32
 <211> 204
 <212> PRT
 <213> Glycine max

<400> 32
 Met Asp Lys Lys Leu Gly Asn Thr Ser His Asp Pro Glu Val Arg Lys
 1 5 10 15

Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Ile Thr Tyr Ile Ala
 20 25 30
 Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly Leu
 35 40 45
 Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg
 50 55 60
 Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile
 65 70 75 80
 Met Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys
 85 90 95
 His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr
 100 105 110
 Arg Ile Gln Lys His Leu Lys Gln Ala Ser Ser Ser Phe Gln Gln Gln
 115 120 125
 Ser Ser Asn Ser Glu Ile Ile Tyr His Pro Gln Ala Cys Thr Ser Gln
 130 135 140
 Val Ser Thr Met Ala Gln Pro Ile Glu Thr Tyr Ser Pro Pro Ser Tyr
 145 150 155 160
 Gln Gly Met Leu Asp Pro Phe Ser Ile Gln Phe Pro Thr Asn Pro His
 165 170 175
 His Ser Ser Cys Cys Thr Asn Asp Asp Asp Asn Asn Asn Tyr Trp Ser
 180 185 190
 Met Glu Asp Ile Trp Ser Met Gln Leu Ala Asn Tyr
 195 200

<210> 33
 <211> 910
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (798)

<220>
 <221> unsure
 <222> (807)

<220>
 <221> unsure
 <222> (814)

<400> 33
 tctctctctc tctctctcta gcgtgcacac aaaataatgg acaaaaaacc atgcgactca 60
 tctcatgata cagaagttag aaagggacca tggatcatgg aagaagactt gatcttgata 120
 aactatattg caaatcacgg tgaaggtgtt tgggaattctt tagccaaagc ttctgggtctt 180
 aaacgaacgg gaaagagttg tcgactccgt tggctaaact accttcgtcc tgatgttaga 240
 agaggaaaca ttacacccga agaacagctt ttgatcatag aacttcatgc aaagtggggc 300
 aataggtggt ccaaaattgc aaagcatctt ccaggaagaa ctgacaatga gattaagaac 360


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ttctggagaa ctaggatcca gaagcacatt aagcaagctg agacttcaca acaacatggt 420
aattcatcag agaatagtaa taatgatcat caagcaagca atagcactag caaggtgtcc 480
accatggcac atccaaatga gactttctct tcaccctcat accaagcaac ttttgagcca 540
tttcaacctc aattcctaca atcaatgata aatcaagttg ttgtaccagc aacaacaact 600
attggagcat cgaggatata tggtcgtcta tgcaattact caatggagat waattaaatc 660
tagctatatg catgcttata taaatcatat atgtgatgat atataaacct aagctcttat 720
tgagtgtggt caggcttaat aacatcatta ggtctggtat atatgagtag gttaagattg 780
gtgtgcatgc ctaaagtagn tattgcntta ttgnagtaag aataactagt tatggatgcc 840
tttaaaaaaa agttagtatt gaattgaaat atatagtaac ttatatacta aaaaaaaaaa 900
aaaaaaaaaa                                     910

```

```

<210> 34
<211> 206
<212> PRT
<213> Glycine max

```

```

<400> 34
Met Asp Lys Lys Pro Cys Asp Ser Ser His Asp Pro Glu Val Arg Lys
  1             5             10             15

```

```

Gly Pro Trp Ile Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile Ala
      20             25             30

```

```

Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ser Gly Leu
      35             40             45

```

```

Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg
      50             55             60

```

```

Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile
      65             70             75             80

```

```

Ile Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys
      85             90             95

```

```

His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Arg Thr
      100            105            110

```

```

Arg Ile Gln Lys His Ile Lys Gln Ala Glu Thr Ser Gln Gln His Gly
      115            120            125

```

```

Asn Ser Ser Glu Asn Ser Asn Asn Asp His Gln Ala Ser Asn Ser Thr
      130            135            140

```

```

Ser Lys Val Ser Thr Met Ala His Pro Asn Glu Thr Phe Ser Ser Pro
      145            150            155            160

```

```

Ser Tyr Gln Ala Thr Phe Glu Pro Phe Gln Pro Gln Phe Leu Gln Ser
      165            170            175

```

```

Met Ile Asn Gln Val Val Val Pro Ala Thr Thr Thr Ile Gly Ala Ser
      180            185            190

```

```

Arg Ile Ser Gly Arg Leu Cys Asn Tyr Ser Met Glu Ile Asn
      195            200            205

```

```

<210> 35
<211> 863
<212> DNA
<213> Glycine max

```

<400> 35
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agatcctgaa gtgagaaaaag ggccttggac aatggaagaa gacttgatct tgatgaacta 120
tattgcaaat catggggaag gtgtttggaa ctctttggcc aaagctgctg gtctcaaacg 180
taacggaaaag agttgccggc taaggtggct aaattacctc cgtcctgatg ttagaagagg 240
gaatattaca cccgaggaac aacttttgat tatggagctc cacgcaaagt ggggaaacag 300
gtgggtccaaa attgccaaagc atctacctgg aaggactgat aatgagatca agaactattg 360
gaggacaagg atccagaagc acatcaagca agctgagaac tttcagcaac agagtagtaa 420
taattctgag ataaatgatc accaagctag cactagccat gtttccacca tggctgagcc 480
catggagatg tattctccac cctgttatca aggaatgtta gagccatttt caactcagtt 540
ccctacaatt aatcctgatc aatccagttg ttgtaccaat gacaacaaca acattaacta 600
ttggagcatg gaggatagct ggtcaatgca attactgaac ggtgattaaa tattatcaag 660
ataaaaccta agttytgaag ttccataagg ctggaatgtc tytggattaa aacatattat 720
tgggtttggt tatataagta gttggatgtt tggttttgcg taccattatt agctatgtgc 780
tgtaatatat acgagatytt atattaaact atatctgcat gctttatata taaaaaaaaa 840
aaaaaaaaa aaaaaaaaaa aaa 863

<210> 36
<211> 206
<212> PRT
<213> Glycine max

<400> 36
Met Asp Lys Lys Gln Gln Cys Lys Thr Ser Gln Asp Pro Glu Val Arg
1 5 10 15
Lys Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Met Asn Tyr Ile
20 25 30
Ala Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly
35 40 45
Leu Lys Arg Asn Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu
50 55 60
Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu
65 70 75 80
Ile Met Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala
85 90 95
Lys His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg
100 105 110
Thr Arg Ile Gln Lys His Ile Lys Gln Ala Glu Asn Phe Gln Gln Gln
115 120 125
Ser Ser Asn Asn Ser Glu Ile Asn Asp His Gln Ala Ser Thr Ser His
130 135 140
Val Ser Thr Met Ala Glu Pro Met Glu Met Tyr Ser Pro Pro Cys Tyr
145 150 155 160
Gln Gly Met Leu Glu Pro Phe Ser Thr Gln Phe Pro Thr Ile Asn Pro
165 170 175
Asp Gln Ser Ser Cys Cys Thr Asn Asp Asn Asn Asn Ile Asn Tyr Trp
180 185 190

Ser Met Glu Asp Ser Trp Ser Met Gln Leu Leu Asn Gly Asp
 195 200 205

<210> 37
 <211> 805
 <212> DNA
 <213> Glycine max

<400> 37
 aaaaaaacat gcaactcatc atctcatgat cctgaagtga gaaagggacc atggaccatg 60
 gaagaagact tgatcttgat aaactatatt gcaaatcacg gtgaagggtg ttggaactcc 120
 ttagccaaag cttctggtct caaacgaacg ggaaagaggt gtcgactccg ttggctaaac 180
 taccttcgtc ctgatgttag aagaggaaac attacacccg aggaacagct ttgatcata 240
 gaacttcacg caaagtggg caataggtgg tccaaaattg caaagcatct tccaggaaga 300
 actgacaatg agattaagaa cttctggaga acaaggatcc aaaagcacat taagcaagct 360
 gagacttcac aacaacatgg taattcagag aataatgatc atcaagcaag cactagtact 420
 agcaaagtgt ccaccatggc acatccaaat gagactttct ctccaccctc ataccaagga 480
 acttttgagc cattccaacc tcaattccct acaatcactg atcaatcaag ttgttgtacc 540
 accaccaacg acaacaacaa ctattggagc atcgaggata tctggtcgtc tatgcaatta 600
 ctcaatggag attaaaccta gctatatgca tgcctatata aatcatatat atgatgatat 660
 ataaacctaa gctctttagt agtgtgttca ggcttaataa catcattagg tctgtttata 720
 tgagtagtct aagtttggtg tttgtaatgc atgatgtgag ttaagaatta atttagttat 780
 ggttggaata aaaaaaaaaa aaaaa 805

<210> 38
 <211> 204
 <212> PRT
 <213> Glycine max

<400> 38
 Lys Lys Pro Cys Asn Ser Ser Ser His Asp Pro Glu Val Arg Lys Gly
 1 5 10 15
 Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile Ala Asn
 20 25 30
 His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ser Gly Leu Lys
 35 40 45
 Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro
 50 55 60
 Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile Ile
 65 70 75 80
 Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys His
 85 90 95
 Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Arg Thr Arg
 100 105 110
 Ile Gln Lys His Ile Lys Gln Ala Glu Thr Ser Gln Gln His Gly Asn
 115 120 125
 Ser Glu Asn Asn Asp His Gln Ala Ser Thr Ser Thr Ser Lys Val Ser
 130 135 140
 Thr Met Ala His Pro Asn Glu Thr Phe Ser Pro Pro Ser Tyr Gln Gly
 145 150 155 160

Thr Phe Glu Pro Phe Gln Pro Gln Phe Pro Thr Ile Thr Asp Gln Ser
165 170 175

Ser Cys Cys Thr Thr Thr Asn Asp Asn Asn Asn Tyr Trp Ser Ile Glu
180 185 190

Asp Ile Trp Ser Ser Met Gln Leu Leu Asn Gly Asp
195 200

<210> 39
<211> 751
<212> DNA
<213> Glycine max

<400> 39
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aaaaggagat gggcatgaga aaaggtccat gggcggttga ggaggacacc attctggtca 120
attacatcgc cacacacggt gaaggccact ggaattccgt ggcacgatgt gcaggtctaa 180
ggaggagtgg gaagagttgc agattaaggt ggctaaacta cttgcgcca gacgtgcggc 240
gtggaaatat cacactccaa gaacaaatat taattctcga ccttcactct cgctggggca 300
acaggtgggc aaagattgct caacagctgc caggaagaac agacaacgaa ataaagaact 360
attggaggac cagagtgata aaacaagcga agcagctaaa gtgcgatgtg aatagcaaac 420
agttcagaga cagttgctg tacgtttgga tgccgcgctt gctggagcgg cttcagccca 480
catcacaagc actggagcca aaccaaagtg gacttgtgtt acacgcttca tcatcactgc 540
ttccttcgaa ttccgaccat agtattgaaa gggggtcggg tctgtggcca ggtttcaata 600
accaaagtgt gttggaacag gggagtggcg gtgacttgtt ggaaagtgtg tgggatgacg 660
acaatatgtg ctttttgcaa cagctttctt atgacctcca aatgaaataa aatacaattc 720
ccttcogtca cgcaaaaaaa aaaaaaaaaa a 751

<210> 40
<211> 235
<212> PRT
<213> Glycine max

<400> 40
Asp Val Lys Lys Gly Gly Ser Val Val Gln Ala Gln Val Lys Leu Gln
1 5 10 15

Lys His Asn Glu Lys Glu Met Gly Met Arg Lys Gly Pro Trp Ala Val
20 25 30

Glu Glu Asp Thr Ile Leu Val Asn Tyr Ile Ala Thr His Gly Glu Gly
35 40 45

His Trp Asn Ser Val Ala Arg Cys Ala Gly Leu Arg Arg Ser Gly Lys
50 55 60

Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg
65 70 75 80

Gly Asn Ile Thr Leu Gln Glu Gln Ile Leu Ile Leu Asp Leu His Ser
85 90 95

Arg Trp Gly Asn Arg Trp Ser Lys Ile Ala Gln Gln Leu Pro Gly Arg
100 105 110

Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr Arg Val Ile Lys Gln
115 120 125

Ala Lys Gln Leu Lys Cys Asp Val Asn Ser Lys Gln Phe Arg Asp Thr
 130 135 140

Leu Arg Tyr Val Trp Met Pro Arg Leu Leu Glu Arg Leu Gln Pro Thr
 145 150 155 160

Ser Gln Ala Leu Glu Pro Asn Gln Ser Gly Leu Val Leu His Ala Ser
 165 170 175

Ser Ser Leu Leu Pro Ser Asn Ser Asp His Ser Ile Glu Arg Gly Ser
 180 185 190

Asp Leu Trp Pro Gly Phe Asn Asn Gln Met Leu Leu Glu Gln Gly Ser
 195 200 205

Gly Gly Asp Leu Leu Glu Ser Leu Trp Asp Asp Asp Asn Met Cys Phe
 210 215 220

Leu Gln Gln Leu Ser Tyr Asp Leu Gln Met Lys
 225 230 235

<210> 41
 <211> 500
 <212> DNA
 <213> Glycine max

<400> 41
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 gagtgaagctg agaagagggtc cttggactct tgaagaagac agcttactca tacactatat 180
 tgctcgtcat ggtgaaggcc gttggaatat gttagccaaa agtgcaggat tgaagaggac 240
 tggaaaaagt tgcagactta gatggctgaa ttatttgaaa ccagacatta agagagggaa 300
 cctcactcca caggagcaac tcttgatcct tgaactccat tccaagtggg gtaacaggtg 360
 gtcaaaaatt gctcagcatc tgccaggaag aacagacaat gagatcaaga actattggag 420
 aacaaggata cagaaacagg gcacgccaac ttaacattga atctggtagc aagagattca 480
 ttgatgctgt cagtgttttt 500

<210> 42
 <211> 229
 <212> PRT
 <213> Glycine max

<220>
 <221> UNSURE
 <222> (138)

<400> 42
 Met Ser Thr Ile Ala Lys Arg Asp Leu Ser Ser Asn Glu Glu Glu Ser
 1 5 10 15

Glu Leu Arg Arg Gly Pro Trp Thr Leu Glu Glu Asp Ser Leu Leu Ile
 20 25 30

His Tyr Ile Ala Arg His Gly Glu Gly Arg Trp Asn Met Leu Ala Lys
 35 40 45

Ser Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu
 50 55 60

Asn Tyr Leu Lys Pro Asp Ile Lys Arg Gly Asn Leu Thr Pro Gln Glu
 65 70 75 80
 Gln Leu Leu Ile Leu Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser
 85 90 95
 Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn
 100 105 110
 Tyr Trp Arg Thr Arg Ile Gln Lys Gln Ala Arg Gln Leu Asn Ile Glu
 115 120 125
 Ser Gly Ser Lys Arg Phe Ile Asp Ala Xaa Lys Cys Phe Trp Met Pro
 130 135 140
 Arg Leu Leu Gln Lys Met Glu Gln Ser Asn Ser Pro Ser Pro His His
 145 150 155 160
 Ser Ser Met Thr Asn Met Met Asn Leu Gly Asn Ser Gly Glu Ala Ser
 165 170 175
 Met Ser Ser Met Ser Ser Ser Phe Asn Ile Asn Pro Ser Met Ser Ser
 180 185 190
 Ser Ser Ser Pro Pro Lys Gly Asn Leu Leu Trp Met Met Pro Asn His
 195 200 205
 Phe Lys Tyr Tyr Val Gln Pro His Gln Ser Ile Pro Arg Phe Leu Pro
 210 215 220
 Ile Phe Thr Ala Thr
 225

<210> 43
 <211> 1348
 <212> DNA
 <213> Glycine max

<400> 43
 tacctctcca accaagacca atttgaaaac ctcttcaatc caacaaacaa acgttctccc 60
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 tagtgaggac gagatggacc ttccaagagg cccttggaac gtgatgaag acctcactct 180
 tatcaattac gttgccactc atggcgaagg tcgctggaat accctcgccc tctctgctgg 240
 gctgaaacga acggggaaga gttgcagatt gaggtggctg aattatctgc gtcctgatgt 300
 tcgacgtgga aacatcacgc ttgaagaaca acttttgatt ctggagctcc attctcgctg 360
 gggaaaccga tggtcgaaaa ttgctcaata tttgcctggt agaaccgaca atgagataaa 420
 gaactattgg agaaccctgt tccaaaagca tgccaagcaa ctcaaatgcg acgtgaatag 480
 caagcaattc aaggacacca tgcgttacat ttggatgcca aggctcgtgg aacgcattca 540
 agccaccgt gccgcctccg caccacaacc cgttaccgta ccaccgcgac caacaatgca 600
 tacacctacg gaagcaacct taataacaac aaattcgagg ttcacgatca caagggcaaa 660
 atgggggttaa ccgatccttc agttatgaac aatgacttaa tgggttcaca tgtcacgcaa 720
 agttacaccc ctgagaatag tagcacgggt gcgtcatcat cagactcgtt tgggactcaa 780
 gtctcagcaa tttctgattt gactgaatat tacactgtca ctggtagtgg taacaataac 840
 aatactaatt ctgcggatta ttatcaaccc tctcaaatta gttactcgga tagttgcata 900
 acaagcccat ctgggttggt ccctcaaggg ctgatttttc aatccatgga tccaaacacc 960
 ccgtggaaca tgcaaagtgg ggactcctct gacagttttt ggaacgttga aagcatgttg 1020
 ttcttagagc agcaactcat gaatgacaac atgtgaaaac attgggaata ggaaaataag 1080
 acctagatac ggttcttctt agtattgtgt ttttaattaaa gttaaagtta acacaagtta 1140
 ttgaagtga accttaattt taattgaata ataatactga aaacaagagt tgtattttaag 1200
 ttttattctt ttatgaatta tgaattagat tgacagaagg ggttgtttgt gaaatatata 1260

ggtgaaagta tagaaagtag caacattaat aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1320
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1348

<210> 44
 <211> 196
 <212> PRT
 <213> Glycine max

<400> 44
 Met Asp Gly Lys Gly Ala Arg Ser Ser Asn Thr Leu Leu Ser Ser Glu
 1 5 10 15
 Asp Glu Met Asp Leu Arg Arg Gly Pro Trp Thr Val Asp Glu Asp Leu
 20 25 30
 Thr Leu Ile Asn Tyr Val Ala Thr His Gly Glu Gly Arg Trp Asn Thr
 35 40 45
 Leu Ala Leu Ser Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu
 50 55 60
 Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr
 65 70 75 80
 Leu Glu Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn
 85 90 95
 Arg Trp Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu
 100 105 110
 Ile Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu
 115 120 125
 Lys Cys Asp Val Asn Ser Lys Gln Phe Lys Asp Thr Met Arg Tyr Ile
 130 135 140
 Trp Met Pro Arg Leu Val Glu Arg Ile Gln Ala Thr Ala Ala Ala Ser
 145 150 155 160
 Ala Pro Gln Pro Val Thr Val Pro Pro Arg Pro Thr Met His Thr Pro
 165 170 175
 Thr Glu Ala Thr Leu Ile Thr Thr Asn Ser Arg Phe Thr Ile Thr Arg
 180 185 190
 Ala Lys Trp Gly
 195

<210> 45
 <211> 1236
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (519)

<220>
 <221> unsure
 <222> (521)

1007011 3170

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<220>
<221>   unsure
<222>   (800)
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<220>
<221>  unsure
<222>  (1151)
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<400>	45						
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aaacttaatt	tcttttgttt	tgagtttctt	agagaatgga	tgaaaaagga	gcaagaagta		120
gcaacaccct	tttaagttgt	gaggacgaga	tggaccttcg	aagaggccct	tggaccgtcg		180
atgaagacct	cactcttata	aattacattg	ccactcatgg	cgaaggctcg	tggaacacgc		240
tctgcccctc	tgctgggctg	aaacgaacgg	ggaagagttg	cagattgagg	tggttgaatt		300
atcgtcgtcg	tgatgttcga	cgtggaaaca	tcacacttga	agaacaactt	ttgattctgg		360
agcttcattc	tcgctgggga	aaccgttggt	cgaaaattgc	tcaatatttg	cctggtagaa		420
ccgacaacga	gataaagaac	tattggagaa	cccgtgtcca	aaagcatgcc	aagcaactca		480
aatgtgacgt	gaatagcaag	caattcaagg	acaccatgng	ntacctttgn	natnccaagg		540
ctcgtggaac	gcattcaagc	agcggcgacg	gcccccgtaa	ccaccaccgt	aactgcggcc		600
gccaccaaca	atgcattcac	ctacggraac	aaccttatac	caccaaattc	gaggttctga		660
atcacaaggg	cagaatgggg	ttaaccgatc	cttcagttgc	gaacaaatgc	tttgtggggt		720
cacatgtcac	gcaaaggtae	ccactcctcg	agaatagtag	cacgggtgcg	tcactcatcg		780
actcgttttg	gactcaagtn	tcaacaattt	ctgatttgac	tgaaaattcc	agtgtccctg		840
aaaataactaa	ttctgcggat	tattatcaac	cctctcaaatt	tagtaattac	tcggataatt		900
gcatcacaag	cccatctggg	ttcttggttc	ctcaaggact	agatcttcaa	tccatggatc		960
caaacacacc	gtggaacatg	caaagtgggg	actcctctga	caattttttg	gacgttgaaa		1020
gcatgttatt	cttagagcag	caactcatga	atgacaacat	gtgaaacatt	gggaatagga		1080
aaataagact	tagatacggg	tcttcttaata	tttttttagtg	ktgngtttta	attaaagtta		1140
aagttaacac	naagtattgt	agtgaaactt	tatttttaata	taaataataa	tcttgaaaaa		1200
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaa				1236

<210>	46
<211>	322
<212>	PRT
<213>	Glycine max

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<220>
<221>  UNSURE
<222>  (145)..(146)..(147)
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<220>
<221> UNSURE
<222> (178)

<400> 46
 Met Asp Glu Lys Gly Ala Arg Ser Ser Asn Thr Leu Leu Ser Cys Glu
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 Asp Glu Met Asp Leu Arg Arg Gly Pro Trp Thr Val Asp Glu Asp Leu
 20 25 30
 Thr Leu Ile Asn Tyr Ile Ala Thr His Gly Glu Gly Arg Trp Asn Thr
 35 40 45
 Leu Ala Leu Ser Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu
 50 55 60
 Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr
 65 70 75 80
 Leu Glu Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn
 85 90 95
 Arg Trp Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu
 100 105 110
 Ile Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu
 115 120 125
 Lys Cys Asp Val Asn Ser Lys Gln Phe Lys Asp Thr Met Xaa Tyr Leu
 130 135 140
 Xaa Xaa Xaa Lys Ala Arg Gly Thr His Ser Ser Ser Gly Asp Gly Pro
 145 150 155 160
 Arg Asn His His Arg Asn Cys Gly Arg His Gln Gln Cys Ile His Leu
 165 170 175
 Arg Xaa Gln Pro Tyr Thr Thr Lys Phe Glu Val Leu Asn His Lys Gly
 180 185 190
 Arg Met Gly Leu Thr Asp Pro Ser Val Ala Asn Asn Asp Phe Val Gly
 195 200 205
 Ser His Val Thr Gln Arg Tyr Pro Thr Pro Glu Asn Ser Ser Thr Gly
 210 215 220
 Ala Ser Ser Ser Asp Ser Phe Gly Thr Gln Val Ser Thr Ile Ser Asp
 225 230 235 240
 Leu Thr Glu Asn Ser Ser Val Pro Glu Asn Thr Asn Ser Ala Asp Tyr
 245 250 255
 Tyr Gln Pro Ser Gln Ile Ser Asn Tyr Ser Asp Asn Cys Ile Thr Ser
 260 265 270
 Pro Ser Gly Phe Leu Phe Pro Gln Gly Leu Asp Leu Gln Ser Met Asp
 275 280 285
 Pro Asn Thr Pro Trp Asn Met Gln Ser Gly Asp Ser Ser Asp Asn Phe
 290 295 300

Trp Asp Val Glu Ser Met Leu Phe Leu Glu Gln Gln Leu Met Asn Asp
 305 310 315 320

Asn Met

<210> 47
 <211> 1181
 <212> DNA
 <213> Glycine max

<400> 47
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 gacaatgaac ttagaagagg gccttggact ctggaagagg ataacttgct ctcccaatat 120
 atttttaatc atggggaagg gcgatggaat ttgctggcta aacgttcagg attaaagaga 180
 actgggaaaa gttgcagatt aaggtggcta aattatctaa agccagatgt aaaacgggga 240
 aatttaaccc cacaagagca acttataatt cttgaactcc actcaaagtg gggaaacagg 300
 tggtcacaaa ttgcacaaca ttggccaggc agaacagaca atgaaatcaa gaactattgg 360
 agaactagga ttcagaaaca agcaagacat ttgaaaatth acactgacag cagagagttt 420
 caagaacttg ttaggcgttt ctggatgcct agattgcttc agaaagcaaa agaatacatc 480
 tcttcaaaca tgtcaattca aaaccaggca attcctatgc cttttgatta tgtttctcag 540
 catttaactg ttgggaccat acctccttgg cagggacott gtatgaatga agctgggtccc 600
 acttacatgg accaacaatga gcagactcag actcggaaca ccaacaatgg ttcattgcac 660
 tccttgtctg agtcagcaaa tattccaaaa gtgcctcagc attttggaca caccaccatc 720
 acccaatttc atgccttgaa taccaatgac ttgggcacct tcacatatga aggtttataat 780
 gtaacaaca atgtctatga gatggacaac ttcaaaacga ctactacatg ggtggctgag 840
 gatgcgcaat acccaattgg tgattgtcaa atggtaggaa gcaattgggt aaacaacgat 900
 ttgcatgta acatgtggaa catggatgaa ctgtggcagt ttagcaagtt acaaaaaataa 960
 gatttttaggg ttttgttttt ttgggaataa ccaaaagtcc aaaactcttt ctttgatgac 1020
 gttattattg ttatcatgaa ctgtggatta gctaccgaat taattaatac agatggcgat 1080
 tgttttctgt acatctgtct tgtattactc tggtcagata agtacttttg taatttgtat 1140
 tgattgagaa aagtcattaa ttagtcacta gtacaaaaaa a 1181

<210> 48
 <211> 312
 <212> PRT
 <213> Glycine max

<400> 48
 Met Ser Thr Ser Lys Ser Val Ser Ser Ser Ser Glu Asp Asp Asn Glu
 1 5 10 15
 Leu Arg Arg Gly Pro Trp Thr Leu Glu Glu Asp Asn Leu Leu Ser Gln
 20 25 30
 Tyr Ile Phe Asn His Gly Glu Gly Arg Trp Asn Leu Leu Ala Lys Arg
 35 40 45
 Ser Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn
 50 55 60
 Tyr Leu Lys Pro Asp Val Lys Arg Gly Asn Leu Thr Pro Gln Glu Gln
 65 70 75 80
 Leu Ile Ile Leu Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser Lys
 85 90 95
 Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr
 100 105 110

Trp Arg Thr Arg Ile Gln Lys Gln Ala Arg His Leu Lys Ile Tyr Thr
 115 120 125
 Asp Ser Arg Glu Phe Gln Glu Leu Val Arg Arg Phe Trp Met Pro Arg
 130 135 140
 Leu Leu Gln Lys Ala Lys Glu Ser Ser Ser Asn Met Ser Ile Gln
 145 150 155 160
 Asn Gln Ala Ile Pro Met Pro Phe Asp Tyr Val Ser Gln His Leu Thr
 165 170 175
 Val Gly Thr Ile Pro Pro Trp Gln Gly Pro Cys Met Asn Glu Ala Gly
 180 185 190
 Pro Thr Tyr Met Asp Gln His Glu Gln Thr Gln Thr Arg Asn Thr Asn
 195 200 205
 Asn Gly Ser Cys Ile Ser Leu Ser Glu Ser Ala Asn Ile Pro Lys Val
 210 215 220
 Pro Gln His Phe Gly His Thr Thr Ile Thr Gln Phe His Ala Leu Asn
 225 230 235 240
 Thr Asn Asp Phe Gly Thr Phe Thr Tyr Glu Gly Tyr Asn Val Asn Asn
 245 250 255
 Asn Val Tyr Glu Met Asp Asn Phe Lys Thr Thr Thr Thr Trp Val Ala
 260 265 270
 Glu Asp Ala Gln Tyr Pro Ile Gly Asp Cys Gln Met Val Gly Ser Asn
 275 280 285
 Trp Val Asn Asn Asp Phe Ala Cys Asn Met Trp Asn Met Asp Glu Leu
 290 295 300
 Trp Gln Phe Ser Lys Leu Gln Lys
 305 310

<210> 49

<211> 1186

<212> DNA

<213> Glycine max

<400> 49

aattcggcac	gaggccatgt	ctacttcaaa	gagcgtcagc	agttctagt	aagatgacaa	60
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tagtcatgga	gaagggcgat	ggaatttgct	agctaaacgt	tcaggattaa	agcgaactgg	180
gaaaagtgtc	agattaaggt	ggctaaatta	tctaaagcca	gatgtaaaac	ggggaaattt	240
aacccacaaa	gagcaactta	taatcctcga	actccactca	aagtggggaa	acaggtgggtc	300
aaaaattgca	caaaatttgc	caggcagaac	agacaatgaa	atcaagaact	attggagaac	360
taggattcag	aaacaagcaa	gacatttgaa	aattgacact	gacaccagag	agtttcagga	420
actgtttagg	cgtttctgga	tgcctagatg	cttcaaaaag	cccaagaatc	atcttcttca	480
gccatgtcaa	ttcaaaacca	ggcaactcct	atgccttttg	atgggtgtttc	tcagcattca	540
actgttgagg	ccataccatc	acattcacac	accccttggtc	agggaccttg	tatgaatgaa	600
gctggtccca	cttacatgga	ccaacatgag	cagaactcag	actctgaaca	caacaatggg	660
tcatgcatct	ccttgtctga	gtcagcaaat	tttccaaaag	tgcctcagca	ttttggacgc	720
accaccatca	cccaatatca	tgccttgaat	aacaatgact	ttggcacctt	cacatatgac	780
ggctacaatg	taagcaacaa	tgtctatgag	atggacaact	tcaaaacgcc	tactacaagg	840
gtggctgagg	atgcgcaata	cccaactggg	gattgtcaaa	tggtaggaag	caattgggta	900

aacagcgatt ttgcatgtaa catgtggaac atggatgaat tgtggcaatt tagcaagtta 960
caaaaataag attttagggg ttgggttttt tggagttacc aagactctat ctttggtgat 1020
gttattattg ttatcatgaa ctgttgatta gctactacca aattaattaa tacagatggg 1080
gattgttttc tgtacatctg ttttgcatta ctctgttttg caatttgtat tgattgagaa 1140
aagtcattaa ttagtcacta gttcaaaaaca caaaaaaaaa aaaaaa 1186

<210> 50
<211> 192
<212> PRT
<213> Glycine max

<400> 50
Met Ser Thr Ser Lys Ser Val Ser Ser Ser Ser Glu Asp Asp Asn Glu
1 5 10 15
Leu Arg Arg Gly Pro Trp Thr Leu Glu Glu Asp Asn Leu Leu Ser Gln
20 25 30
Tyr Ile Ser Ser His Gly Glu Gly Arg Trp Asn Leu Leu Ala Lys Arg
35 40 45
Ser Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn
50 55 60
Tyr Leu Lys Pro Asp Val Lys Arg Gly Asn Leu Thr Pro Gln Glu Gln
65 70 75 80
Leu Ile Ile Leu Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser Lys
85 90 95
Ile Ala Gln Asn Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr
100 105 110
Trp Arg Thr Arg Ile Gln Lys Gln Ala Arg His Leu Lys Ile Asp Thr
115 120 125
Asp Thr Arg Glu Phe Gln Glu Leu Val Arg Arg Phe Trp Met Pro Arg
130 135 140
Cys Phe Lys Lys Pro Lys Asn His Leu Leu Gln Pro Cys Gln Phe Lys
145 150 155 160
Thr Arg Gln Leu Leu Cys Leu Leu Met Val Phe Leu Ser Ile Gln Leu
165 170 175
Leu Gly Pro Tyr His His Ile His Thr Pro Leu Gly Arg Asp Leu Val
180 185 190

<210> 51
<211> 487
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (358)

<220>
<221> unsure
<222> (429)

<400> 51
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aattagaagg acagccacaa gtataaaggc ggtgaaataa aagagaaaga caagaaggag 180
acatgggaag accaccttgt tgtgacaaag aaggggtcaa gaaagggcct tggactcctg 240
aagaagacat catattggtg tcttatattc aggaacatgg tcctggaaat tggagggcag 300
ttcctgccaa aacaggggtg tcaagatgca gcaagagttg cagacttaga tggacgantt 360
acctgaggcc aggaatcaag cgtggtaact tcacaagaac aagaggagaa gatgataatc 420
catcttcang atcttttagg aaacagatgg ggtgcaatag cttcatacct tccacaaagg 480
acaaggg 487

<210> 52
<211> 90
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (59)

<220>
<221> UNSURE
<222> (72)

<220>
<221> UNSURE
<222> (83)

<400> 52
Met Gly Arg Pro Pro Cys Cys Asp Lys Glu Gly Val Lys Lys Gly Pro
1 5 10 15
Trp Thr Pro Glu Glu Asp Ile Ile Leu Val Ser Tyr Ile Gln Glu His
20 25 30
Gly Pro Gly Asn Trp Arg Ala Val Pro Ala Lys Thr Gly Leu Ser Arg
35 40 45
Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Xaa Tyr Leu Arg Pro Gly
50 55 60
Ile Lys Arg Gly Asn Phe Thr Xaa Glu Gln Glu Glu Lys Met Ile Ile
65 70 75 80
His Leu Xaa Asp Leu Leu Gly Asn Arg Trp
85 90

<210> 53
<211> 1556
<212> DNA
<213> Glycine max

<400> 53
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cacacataga tagagagagg aaaacgacct atattttttt tcctttgaga gcttcagggg 120
ctaggaaaaat tagaaggaca gccacaagta taaaggcggg gaaataaaaag agaaagacaa 180
gaaggagaca tgggaagacc accttggtgt gacaaagaag gggcgaagaa agggccttgg 240
actcctgaag aagacatcat attggtgtct tatattcagg aacatgggtc tggaaattgg 300
agggcagttc ctgccaaaac aggggtgtca agatgcagca agagtgcag acttagatgg 360

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acgaattacc tgaggccagg aatcaagcgt ggtaacttca cagaacaaga ggagaagatg 420
ataatccatc ttcaagatct tttaggaaac agatgggctg caatagcttc ataccttcca 480
caaagaacag acaatgacat aaagaactat tggaataccc atttgagaaa gaagctgaag 540
aagatgcaag caggcggtga aggtggttagc tttggagaag ggttttcagc ctcaaggcaa 600
atccctagag gccagtggga aagaaggctc caaactgata tccaaatggc aaagagagcc 660
ctcagtgaag ctctttcacc agagaaaaag ccatcttggt tatctgcctc aaactcaaac 720
ccttcagata gtagcagctc ctctctctcc acaaaaccaa caacaacaca atctgtgtgc 780
tatgcatcaa gtgctgacaa catagctaga atgctcaagg gttggatgaa gaaccacca 840
aagtcctcaa gaaccaactc gtctatgact cagaactcat tcaacaactt agcaggtgct 900
gatactgctt gtagtagtgg agcaaaggga ccactaagca gtgccgaatt gtctgagaat 960
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attgctgcag aaattatgcc ctctctcttg cttgagaaat ggctccttga tgaggcaggt 1140
tgccaagaga aattagtggg ttggttggtg gatgccaaagt ttttctaagt tgggttcatt 1200
ttgtgacata tgagactgtg ggattttttt attttatttt attttatttc ataagttata 1260
ggtagggcct catcaattaa tctcgcttcg gccttattag agagagaagt tttccagcct 1320
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tgttagttag catacactgg caaacttgct tctcttatgt aaagttgatc ttgcgacgag 1440
atcctgcttt atggctttag gcagcgcgac cggctcttct tctttgtgtc gcttgattag 1500
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<210> 54
<211> 332
<212> PRT
<213> Glycine max

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<400> 54
Met Gly Arg Pro Pro Cys Cys Asp Lys Glu Gly Val Lys Lys Gly Pro
 1          5          10          15

Trp Thr Pro Glu Glu Asp Ile Ile Leu Val Ser Tyr Ile Gln Glu His
      20          25          30

Gly Pro Gly Asn Trp Arg Ala Val Pro Ala Lys Thr Gly Leu Ser Arg
      35          40          45

Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly
      50          55          60

Ile Lys Arg Gly Asn Phe Thr Glu Gln Glu Glu Lys Met Ile Ile His
      65          70          75          80

Leu Gln Asp Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu
      85          90          95

Pro Gln Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr His Leu
     100          105          110

Arg Lys Lys Leu Lys Lys Met Gln Ala Gly Gly Glu Gly Gly Ser Phe
     115          120          125

Gly Glu Gly Phe Ser Ala Ser Arg Gln Ile Pro Arg Gly Gln Trp Glu
     130          135          140

Arg Arg Leu Gln Thr Asp Ile Gln Met Ala Lys Arg Ala Leu Ser Glu
     145          150          155          160

Ala Leu Ser Pro Glu Lys Lys Pro Ser Cys Leu Ser Ala Ser Asn Ser
     165          170          175

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Asn Pro Ser Asp Ser Ser Ser Ser Phe Ser Ser Thr Lys Pro Thr Thr
 180 185 190
 Thr Gln Ser Val Cys Tyr Ala Ser Ser Ala Asp Asn Ile Ala Arg Met
 195 200 205
 Leu Lys Gly Trp Met Lys Asn Pro Pro Lys Ser Ser Arg Thr Asn Ser
 210 215 220
 Ser Met Thr Gln Asn Ser Phe Asn Asn Leu Ala Gly Ala Asp Thr Ala
 225 230 235 240
 Cys Ser Ser Gly Ala Lys Gly Pro Leu Ser Ser Ala Glu Leu Ser Glu
 245 250 255
 Asn Asn Phe Glu Ser Leu Phe Asp Phe Asp Gln Ser Leu Glu Ser Ser
 260 265 270
 Asn Ser Asp Gln Phe Ser Gln Ser Leu Ser Pro Glu Ala Thr Val Leu
 275 280 285
 Gln Asp Glu Ser Lys Pro Asp Ile Asn Ile Ala Ala Glu Ile Met Pro
 290 295 300
 Phe Ser Leu Leu Glu Lys Trp Leu Leu Asp Glu Ala Gly Cys Gln Glu
 305 310 315 320
 Lys Leu Val Gly Cys Cys Gly Asp Ala Lys Phe Phe
 325 330

<210> 55
 <211> 357
 <212> DNA
 <213> Triticum aestivum

<220>
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 <222> (259)

<220>
 <221> unsure
 <222> (307)

<220>
 <221> unsure
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 ctctgtaatc tccatgcagg cctcaaccgc acaggaaaga gctgtcgctt ccggtggggt 180
 aactacctcc accctgggcc taaagcgtgg gcgcatgact ccccatgaaa gaacgcctca 240
 tcctccaact ccatgctcng tggggaaaca agtgggtccaa ggataacacg gaactgccaa 300
 ggcgtancga caatgaatna aagaactact gggagaacac atttgaggaa aaggaag 357

<210> 56
 <211> 54
 <212> PRT
 <213> Triticum aestivum

<220>
 <221> UNSURE
 <222> (21)

<220>
 <221> UNSURE
 <222> (27)..(28)

<220>
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 <222> (41)

<400> 56
 Ala Gly Leu Asn Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Val Asn
 1 5 10 15
 Tyr Leu His Pro Xaa Leu Lys Arg Gly Arg Xaa Xaa Pro Met Lys Glu
 20 25 30
 Arg Leu Ile Leu Gln Leu His Ala Xaa Trp Gly Asn Lys Trp Ser Lys
 35 40 45

Asp Asn Thr Glu Leu Pro
 50

<210> 57
 <211> 1072
 <212> DNA
 <213> Triticum aestivum

<400> 57
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 cttcaacctc tgtaatctcc atgcaggcct caaccgcaca ggaaagagct gtgcgctccg 180
 gtgggttaac tacctccacc ctggcctaaa gcgtgggcgc atgactcccc atgaagaacg 240
 cctcatcctc gagctccatg ctcggtgggg aaacagggtg tccaggatag cacggaagct 300
 gccagggcgt accgacaatg agatcaagaa ctactggaga acacatatga ggaagaaagc 360
 acaggagagg aagaggagcg tgtcacccctc accatcttca tcctcagtga cataccaatc 420
 cattcagcca cagacgccat cgatcatggg aattggcgag cagggaactc atgggtggcag 480
 tagctgcata acaagcatat tgaagggcac gcctgctgac atggatggat acctcatgga 540
 tcagatatgg atggagattg aggcaccctc tgggggtcaac tttcatgacg ggaaggataa 600
 ttcatacagc agcccctctg gccctctgct gccatcaccc atgtgggatt actacagccc 660
 tgaggcaggc tggaagatgg atgagataaa gatggcccca caagttagct acagtaaagg 720
 aattggcccc agttattgaa gccatatata ttgtatcaga ttactaagtt acttgcaacc 780
 tagcagaagt gaaatgcttt tgttgaaaga accattagca tggatctaaa aaatatttat 840
 atctatctag cattccaagt gtgctcatgt tttatgtatc tactatgtag catctagtgt 900
 gcaagacatg taatgcaagg acacttccac tttgtattca caataatcag ctatctcctg 960
 taagactttt ccaatgcaaa catgattagc aggtgtaata tcaacttaaa tgcttgccaa 1020
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1072

<210> 58
 <211> 198
 <212> PRT
 <213> Triticum aestivum

<400> 58
 Ala Gly Leu Asn Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Val Asn
 1 5 10 15

Tyr Leu His Pro Gly Leu Lys Arg Gly Arg Met Thr Pro His Glu Glu
 20 25 30
 Arg Leu Ile Leu Glu Leu His Ala Arg Trp Gly Asn Arg Trp Ser Arg
 35 40 45
 Ile Ala Arg Lys Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr
 50 55 60
 Trp Arg Thr His Met Arg Lys Lys Ala Gln Glu Arg Lys Arg Ser Val
 65 70 75 80
 Ser Pro Ser Pro Ser Ser Ser Ser Val Thr Tyr Gln Ser Ile Gln Pro
 85 90 95
 Gln Thr Pro Ser Ile Met Gly Ile Gly Glu Gln Glu Leu His Gly Gly
 100 105 110
 Ser Ser Cys Ile Thr Ser Ile Leu Lys Gly Thr Pro Ala Asp Met Asp
 115 120 125
 Gly Tyr Leu Met Asp Gln Ile Trp Met Glu Ile Glu Ala Pro Ser Gly
 130 135 140
 Val Asn Phe His Asp Gly Lys Asp Asn Ser Tyr Ser Ser Pro Ser Gly
 145 150 155 160
 Pro Leu Leu Pro Ser Pro Met Trp Asp Tyr Tyr Ser Pro Glu Ala Gly
 165 170 175
 Trp Lys Met Asp Glu Ile Lys Met Ala Pro Gln Val Ser Tyr Ser Lys
 180 185 190
 Gly Ile Gly Pro Ser Tyr
 195

<210> 59
 <211> 521
 <212> DNA
 <213> Triticum aestivum

 <220>
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 <220>
 <221> unsure
 <222> (355)

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 Pro Trp Thr Val Asp Glu Asp Leu Thr Leu Ile Asn Tyr Ile Ala Asp
 35 40 45
 His Gly Glu Gly Arg Trp Asn Ala Leu Ala Arg Ala Ala Gly Leu Arg
 50 55 60
 Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro
 65 70 75 80
 Asp Val Lys Arg Gly Asn Phe Thr Ala Asp Glu Gln Leu Leu Ile Leu
 85 90 95
 Asp Leu His Ser Arg Trp Gly Asn Arg Trp Ser Lys Xaa Ala Xaa His
 100 105 110
 Leu Pro Gly Arg Thr Asp Asn Glu Asp Xaa Arg Thr Thr Gly Arg Thr
 115 120 125
 Xaa Val Gln
 130

<210> 61
 <211> 464
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> unsure
 <222> (435)

<220>
 <221> unsure
 <222> (442)

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<220>
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<400> 61
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 ggcaactggc ggcgcgtccc caccaggacc ggctgatgc ggtgtagcaa gagctgccgg 180
 ctccggtgga ccaactacct gcgcccaggg atcaagcgcg gcaacttcac cgaccaggag 240
 gagaagctca tcgtccacct ccaggcgtg ctcggaaca ggtgggcccgc gatcgctctc 300
 tacctccccg agcgacccga caacgacatc aagaactact ggaacacgca actcaagcgc 360
 aagctgcaag cggggggcga cgccgcgggc aaaccggcgg cgcaaaggct gctcctcctc 420
 aaagggaat ggganaggcg gngcagacgn catcaanatg cgcc 464

<210> 62
 <211> 122
 <212> PRT
 <213> Triticum aestivum

<400> 62

Met Gly Arg Pro Pro Cys Cys Asp Lys Glu Gly Val Lys Lys Gly Pro
1 5 10 15

Trp Thr Pro Glu Glu Asp Leu Val Leu Val Ser Tyr Val Gln Glu His
20 25 30

Gly Pro Gly Asn Trp Arg Ala Val Pro Thr Arg Thr Gly Leu Met Arg
35 40 45

Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly
50 55 60

Ile Lys Arg Gly Asn Phe Thr Asp Gln Glu Glu Lys Leu Ile Val His
65 70 75 80

Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu
85 90 95

Pro Glu Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr Gln Leu
100 105 110

Lys Arg Lys Leu Gln Ala Gly Gly Asp Ala
115 120

<210> 63

<211> 217

<212> PRT

<213> Pisum sativum

<400> 63

Met Asp Lys Lys Pro Cys Asn Ser Ser Gln Asp Pro Glu Val Arg Lys
1 5 10 15

Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile Ala
20 25 30

Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly Leu
35 40 45

Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg
50 55 60

Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile
65 70 75 80

Met Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys
85 90 95

His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Arg Thr
100 105 110

Arg Ile Gln Lys His Ile Lys Gln Val Asp Asn Pro Asn Gln Gln Asn
115 120 125

Phe Gln Gln Lys Met Ser Leu Glu Ile Asn Asp His His His His His
130 135 140

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Pro	His	Gln	Pro	Ser	Ser	Gln	Val	Ser	Asn	Leu	Val	Glu	Pro	Met	
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Glu	Thr	Tyr	Ser	Pro	Thr	Ser	Tyr	Gln	Gly	Thr	Leu	Glu	Pro	Phe	Pro
				165					170					175	
Thr	Gln	Phe	Pro	Thr	Ile	Asn	Asn	Asp	His	His	Gln	Asn	Ser	Asn	Cys
			180					185					190		
Cys	Ala	Asn	Asp	Asn	Asn	Asn	Asn	Asn	Tyr	Trp	Ser	Met	Glu	Asp	Ile
		195						200				205			
Trp	Ser	Met	Gln	Leu	Leu	Asn	Gly	Asp							
	210					215									

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